

<110> Beinkowski et al.

<120> ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR

<130> 28341/6280M

<140>

<141>

<150> 09/416,901

<151> 1999-10-13

<150> 60/155,493

<151> 1999-09-23

<150> 09/404,133

<151> 1999-09-23

<150> PCT/US99/20881

<151> 1999-09-23

<150> 60/101,594

<151> 1998-09-24

<160> 73

<170> PatentIn Ver. 2.0

 $\langle 210 \rangle$ 1

<211> 1804

<212> DNA

<213> Homo sapiens

<400> 1

atgggcgcac	tggccccggg	gctgctgctg	ctctgctg	cccagtggct	cctgcgcgcc	60
gccccggagc	tggcccccg	gcccttcacg	ctgccccctc	gggtggccgc	ggccacgaac	120
cgcgtagttg	cgcccacccc	gggaccggg	acccctgccc	agcgccacgc	cgacggcttg	180
gcgctcgccc	tggagcctgc	cctggcgctc	cccgccgggc	ccgccaactt	cttggccatg	240
gtagacaacc	tgcaggggga	ctctggccgc	ggctactacc	tggagatgct	gatcgggacc	300
cccccgcaga	agctacagat	tctcgttgac	actggaagca	gtaaactttg	ctgtggcagga	360
accccgcact	cctacataga	cacgtacttt	gacacagaga	ggtctagcac	ataccgcctc	420
aagggctttg	acgtcacagt	gaagtacaca	caagggaagt	ggacgggctt	cgttggggaa	480
gacctcgta	ccatcccca	aggcttcaat	acttcttttc	ttgtcaacat	tgccactatt	540
tttgaatcag	agaattttct	tttgcctggg	attaaattga	atggaaatact	tggcctagct	600
tatgccacac	ttgccaagcc	atcaagttct	ctggagaact	tcttcgactc	cctggtgaca	660
caagcaaa	tccccaacgt	tttctcctatg	cagatgtgtg	gagccggctt	gcccgttgct	720
ggatctggga	ccaacggagg	tagtcttgct	ttgggtggaa	ttgaaccaag	tttgtataaa	780
ggagacatct	ggtatacccc	tattaaggaa	gagtggta	accagataga	aattctgaaa	840
ttggaaattg	gaggccaaag	ccttaatctg	gactgcagag	agtataacgc	agacaaggcc	900
atcgtggaca	gtggcaccac	gctgctgcgc	ctgcccacaga	aggtgtttga	tgcggtgggtg	960
gaagctgtgg	ccgcgcgcat	tctgattcca	gaattctctg	atggtttctg	gactgggtcc	1020
cagctggcgt	gctggacgaa	ttcggaacca	ccttggctct	acttccctaa	aatctccatc	1080
tacctgagag	atgagaactc	cagcaggta	ttccgtatca	caatcctgcc	tcagctttac	1140
attcagccca	tgatgggggc	cggcctgaat	tatgaatgtt	accgattcgg	catttcccca	1200
tccacaaatg	cgctggtgat	cggtgccacg	gtgatggagg	gcttctacgt	catcttcgac	1260
agagcccaga	agagggtggg	cttcgcagcg	agccccgtg	cagaaattgc	aggtgtctga	1320
gtgtctgaaa	tttcggggcc	tttctcaaca	gaggatgtag	ccagaactcg	tgtccccgct	1380
cagctcttga	gcgagcccat	tttctggatt	gtgtccatag	cgtctatgag	cgtctgtgga	1440
gccatcctcc	tttgtctaat	cgtcctgtctg	ctgctgccgt	tccggtgtca	gcgtcgcccc	1500

cgtgaccctg	aggtcgtcaa	tgatgagtc	tctctgggtca	gacatcgctg	gaaatgaata	1560
gccaggcctg	acctcaagca	accatgaact	cagctattaa	gaaaatcaca	tttccagggc	1620
agcagccggg	atcgatggtg	gcgctttctc	ctgtgccac	ccgtcttcaa	tctctgttct	1680
gctcccagat	gccttctaga	ttcactgtct	tttgattctt	gattttcaag	ctttcaaatc	1740
ctccctactt	ccaagaaaaa	taattaaaaa	aaaaacttca	ttctaaacca	aaaaaaaaaa	1800
aaaa						1804

```
<210> 2
<211> 518
<212> PRT
<213> Homo sapiens
```

```
<400> 2
Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
  1                               10                      15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
    20                          25                      30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
    35                          40                      45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
    50                          55                      60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
    65                          70                      75                      80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
          85                          90                      95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
      100                          105                      110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
   115                          120                      125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
   130                          135                      140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
   145                          150                      155                      160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
          165                          170                      175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
      180                          185                      190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
     195                          200                      205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
     210                          215                      220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
   225                          230                      235                      240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
          245                          250                      255
```

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
260 265 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
275 280 285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
290 295 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
305 310 315 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
355 360 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
370 375 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
450 455 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
485 490 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
500 505 510

Val Arg His Arg Trp Lys
515

<210> 3
<211> 2070
<212> DNA
<213> Homo sapiens

<400> 3
atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgct gcctgcccac 60
ggcaccacagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctggggg 120
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240

gtgggcagcc	ccccgcagac	gctcaacatc	ctgggtggata	caggcagcag	taactttgca	300
gtgggtgctg	ccccccaccc	cttcctgcat	cgctactacc	agaggcagct	gtccagcaca	360
taccgggacc	tccggaaggg	tgtgtatgtg	ccctacaccc	agggcaagtg	ggaaggggag	420
ctgggcaccg	acctggttaag	catcccccat	ggccccaacg	tactgtgctg	tgccaacatt	480
gctgccatca	ctgaatcaga	caagttcttc	atcaacggct	ccaactggga	aggcatcctg	540
gggtctggcct	atgctgagat	tgccaggcct	gacgactccc	tggagccttt	ctttgactct	600
ctggtaaaagc	agaccacagt	tcccaacctc	ttctccctgc	acctttgtgg	tgtggctctc	660
cccctcaacc	agtctgaagt	gctggcctct	gtcggaggga	gcatgatcat	tggaggatc	720
gaccactcgc	tgtacacagg	cagtctctgg	tatacaccca	tccggcggga	gtggtattat	780
taggctcatc	ttgtcggggt	ggagatcaat	ggacaggatc	tgaaaatgga	ctgcaaggag	840
tacaactatg	acaagagcat	tgtggacagt	ggcaccacca	accttcggtt	gcccagaaga	900
gtgtttgaag	ctgcagtcaa	atccatcaag	gcagcctcct	ccacggagaa	gttcctctgat	960
ggttttctggc	taggagagca	gctggtgtgc	tggcaagcag	gcaccacccc	ttggaacatt	1020
ttcccagtc	tctcactcta	cctaattgggt	gaggttacca	accagtcctt	ccgcatcacc	1080
atccttccgc	agcaataacct	gcggccagtg	gaagatgtgg	ccacgtccca	agacgactgt	1140
tacaagtttg	ccatctcaca	gtcatccacg	ggcactgtta	tgggagctgt	tatcatggag	1200
ggctttctacg	ttgtctttga	tcggggccga	aaacgaattg	gctttgtctg	cagcgcttgc	1260
catgtgcacg	atgagttcag	gacggcagcg	gtggaaggcc	cttttgtcac	cttggacatg	1320
gaagactgtg	gctacaacat	tccacagaca	gatgagtcaa	ccctcatgac	catagcctat	1380
gtcatggctg	ccatctgcgc	cctcttcatg	ctgccactct	gcctcatggg	gtgtcagtgg	1440
cgctgcctcc	gctgcctgcg	cccagcagct	gatgactttg	ctgatgacat	ctccctgctg	1500
aagtgaggag	gcccattggg	agaagataga	gattccccct	gaccacacct	ccgtggttca	1560
ctttggctcac	aagtaggaga	cacagatggc	acctgtggcc	agcgacctc	aggaccctcc	1620
ccaccaccca	aatgcctctg	ccttgatgga	gaaggaaaag	gtggcaagg	tgggtccag	1680
ggactgtacc	tgtaggaaac	agaaaagaga	agaaagaagc	actctgctgg	cgggaaact	1740
cttggctcacc	tcaaattta	gtcgggaaat	tctgctgctt	gaaacttcag	ccctgaacct	1800
ttgtccacca	ttcctttaaa	ttctccaacc	caaagtattc	ttttttctt	agtttcagaa	1860
gtactggcat	cacacgcagg	ttaccttggc	gtgtgtccct	gtggtaccct	ggcagagaag	1920
agaccaagct	tgtttcctg	ctggccaaag	tcagtaggag	aggatgcaca	gtttgtctat	1980
tgcttttagag	acagggactg	tataaacaag	cctaactattg	gtgcaaagat	tgccctctga	2040
attaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa				2070

```
<210> 4
<211> 501
<212> PRT
<213> Homo sapiens
```

```

<400> 4
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
  1                               10                      15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
      20                      25                      30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
      35                      40                      45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
      50                      55                      60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
      65                      70                      75                      80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
      85                      90                      95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
      100                      105                      110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
      115                      120                      125

```

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205
 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430
 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445
 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
 450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
500

```
<210> 5
<211> 1977
<212> DNA
<213> Homo sapiens
```

<400>	5						
atggcccaag	ccctgccctg	gctcctgctg	tggatgggcg	cgggagtgt	gcctgccac	60	
ggcaccacagc	acggcatccg	gctgccctg	cgcagcggcc	tggggggcgc	ccccctggg	120	
ctgcggctgc	cccgggagac	cgacgaagag	cccaggagc	ccggccggag	gggcagcttt	180	
gtggagatgg	tggacaacct	gaggggcaag	tcggggcagg	gctactacgt	ggagatgacc	240	
gtgggcagcg	ccccgcagac	gctcaacatc	ctggtggata	caggcagcag	taactttgca	300	
gtgggtgctg	ccccccacc	ctctctgcat	cgctactacc	agaggcagct	gtccaggcaca	360	
taccgggacc	tccggaagg	tgtgtatgtg	ccctacacc	agggcaagt	ggaaggggag	420	
ctgggcaccg	acctggtaag	catccccc	ggccccaacg	tcactgtgct	tgccaacatt	480	
gctgccatca	ctgaatcaga	caagtctctc	atcaacggct	ccaactggga	aggcatcctg	540	
gggctggcct	atgctgagat	tgccaggctt	tgtggtgctg	gcttccccct	caaccagtct	600	
gaagtgtctg	cctctgtcgg	agggagcatg	atcattggag	gtatcgacca	ctcgctgtac	660	
acaggcagtc	tctggtatac	acccatccg	cgggagtgtg	attatgaggt	gatcatttgt	720	
cggggtggaga	tcaatggaca	ggtactgaaa	atggactgca	aggagtacaa	ctatgacaa	780	
agcatttgtg	acagtggcac	caccaacctt	cgtttgccca	agaaagtgtt	tgaagtgcga	840	
gtcaaatacca	tcaaggcagc	ctcctccacg	gagaagttcc	ctgatggttt	ctggctagga	900	
gagcagctgg	tgtgctggca	agcaggcacc	accccttgga	acattttccc	agtcattctca	960	
ctctacctaa	tgggtgaggt	taccaaccag	tccttccgca	tcaccatcct	tccgcagcaa	1020	
tacctgcggc	cagtggaaag	tgtggccacg	tcccaagacg	actgttacaa	gtttgccatc	1080	
tcacagtcac	ccacgggcac	tgttatggga	gctgttatca	tggagggtct	ctacgttgtc	1140	
tttgatcggg	cccgaataacg	aattggcttt	gctgtcacgc	cttgccatgt	gcacgatgag	1200	
ttcaggacgg	cagcggtgga	aggccctttt	gtcaccttgg	acatggaaga	ctgtggctac	1260	
aacattccac	agacagatga	gtcaaccctc	atgaccatag	cctatgtcat	ggctgccatc	1320	
tgcgccctct	tcatgtgcgc	actctgcctc	atggtgtgtc	agtggcgctg	cctccgctgc	1380	
ctgcgccagc	agcatgatga	ctttgtgtat	gacatctccc	tgctgaagtg	aggaggccca	1440	
tgggcagaag	atagagattc	ccctggacca	cacctccgtg	gttcactttg	gtcacaagta	1500	
ggagacacag	atggcacctg	tggccagagc	acctcaggac	ctccccacc	caccaaatgc	1560	
ctctgccttg	atggagaagg	aaaaggctgg	caaggtgggt	tccagggact	gtacctgtag	1620	
gaacaagaaa	agagaagaaa	gaagcactct	gctggcggga	atactcttgg	tcacctcaaa	1680	
tttaagtctg	gaaattctgc	tgcttgaaac	ttcagccctg	aacctttgtc	caccattcct	1740	
ttaaattctc	caacccaaga	tattcttctt	ttcttagttt	cagaagtact	ggcatcacac	1800	
gcaggttacc	ttggcgctgt	tcctgtgggt	acctggcag	agaagagacc	aagcttgttt	1860	
ccctgctggc	caaagtcagt	aggagaggat	gcacagtttg	ctatttgctt	tagagacagg	1920	
gactgtataa	acaagcctaa	cattggtgca	aagattgcct	cttgaaaaaa	aaaaaaa	1977	

```
<210> 6
<211> 476
<212> PRT
<213> Homo sapiens
```

<400> 6

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300
 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320
 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335
 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365

- 8 -

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
420 425 430

Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
435 440 445

Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
450 455 460

His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
465 470 475

<210> 7

<211> 2043

<212> DNA

<213> Mus musculus

<400> 7

atggccccag	cgctgcactg	gctcctgcta	tgggtgggct	cggaatgct	gcctgcccag	60
ggaacccatc	tcggcatccg	gctgcccctt	cgcagcggcc	tggcagggcc	acccctgggc	120
ctgaggctgc	cccgggagac	tgacgaggaa	tcggaggagc	ctggccggag	aggcagcttt	180
gtggagatgg	tggacaacct	gaggggaaag	tccggccagg	gctactatgt	ggagatgacc	240
gtaggcagcc	ccccacagac	gctcaacatc	ctggtggaca	cgggcagtag	taactttgca	300
gtgggggctg	ccccacaccc	tttcctgcat	cgctactacc	agaggcagct	gtccagcaca	360
tatcgagacc	tccgaaaggg	tgtgtatgtg	ccctacaccc	agggcaagtg	ggagggggaa	420
ctgggcaccg	acctgggtgag	catccctcat	ggccccaacg	tcactgtgcg	tgccaacatt	480
gctgccatca	ctgaatcgga	caagtctctc	atcaatggtt	ccaactggga	gggcaccta	540
gggctggcct	atgctgagat	tgccaggccc	gacgactctt	tggagccctt	ctttgactcc	600
ctgggtgaag	agaccacacat	tcccaacatc	ttttccctgc	agctctgtgg	cgctggcttc	660
cccctcaacc	agaccgaggc	actggcctcg	gtgggaggga	gcatgatcat	tgggtgtatc	720
gaccactcgc	tatacacggg	cagtctcttg	tacacaccca	tccggcggga	gtggtattat	780
gaagtgatca	ttgtacgtgt	ggaaatcaat	ggtcaagatc	tcaagatgga	ctgcaaggag	840
tacaactacg	acaagagcat	tgtggacagt	gggaccacca	accttcgctt	gcccagaaa	900
gtatttgaag	ctgccgtcaa	gtccatcaag	gcagcctcct	cgacggagaa	gttcccggat	960
ggctttttgg	taggggagca	gctgggtgtg	tggcaagcag	gcacgacccc	ttggaacatt	1020
ttcccagtc	tttcacttta	cctcatgggt	gaagtcacca	atcagtcctt	ccgcatcacc	1080
atccttcttc	agcaatacct	acggccgggtg	gaggacgtgg	ccacgtccca	agacgactgt	1140
tacaagttcg	ctgtctcaca	gtcatccacg	ggcactgtta	tgggagccgt	catcatggaa	1200
ggtttctatg	tcgtcttcga	tcgagcccga	aagcgaattg	gctttgctgt	cagcgttgc	1260
catgtgcacg	atgagttcag	gacggcggca	gtggaagggtc	cgtttggttac	ggcagacatg	1320
gaagactgtg	gctacaacat	tccccagaca	gatgagtc	cacttatgac	catagcctat	1380
gtcatggcgg	ccatctgcgc	cctcttcatg	ttgccactct	gcctcatggt	atgtcagttg	1440
cgctgcctgc	gttgccctgcg	ccaccagcac	gatgactttg	ctgatgacat	ctccctgctc	1500
aagtaaggag	gctcgtgggc	agatgatgga	gacgcccctg	gaccacatct	gggtggttcc	1560
ctttggtcac	atgagttgga	gctatggatg	gtacctgtgg	ccagagcacc	tcaggaccct	1620
caccaacctg	ccaatgcttc	tggcgtgaca	gaacagagaa	atcaggcaag	ctggattaca	1680
gggcttgac	ctgtaggaca	caggagaggg	aagggaagcag	cgttctggtg	gcaggaatat	1740
ccttaggcac	cacaaacttg	agttggaaat	tttgctgctt	gaagcttcag	ccctgaccct	1800
ctgccagca	tcctttagag	tctccaacct	aaagtattct	ttatgtcctt	ccagaagtac	1860
tggcgtcata	ctcaggctac	ccggcatgtg	tccctgtggt	accctggcag	agaaagggcc	1920
aatctcattc	cctgctggcc	aaagtcagca	gaagaagggtg	aagtttgcca	gttgctttag	1980
tgatagggac	tgagactca	agcctacact	ggtacaaaga	ctgcgtcttg	agataaaca	2040
gaa						2043

<400> 8
Met Ala Pro Ala Leu His Trp Leu Leu Leu Trp Val Gly Ser Gly Met
1 5 10 15
Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30
Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45
Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
195 200 205
Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220
Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285
Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
500

<210> 9
<211> 2088
<212> DNA
<213> Homo sapiens

<400> 9
atgctgccccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccactgatg gtaatgctgg cctgctggct gaacccaga ttgcctatgt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
acctgcattg ataccaagga aggcacccctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtaccca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagtgg 360
gagtttgtaa gtgatgccct tctcgttccct gacaagtgca aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcaactgg cacaccgtcg ccaaagagac atgcagtgg 480
aagagtacca acttgcattg ctacggcatg ttgctgccct gcggaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaaagt acaatgtgga ttctgctgat 600
gaggaggagg atgactcggg tgtctggtgg ggaggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt 900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960
gagaggettg aggccaaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020

```

gcagaacgctc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080
caggagaaaag tggaaatcttt ggaacaggaa gcagccaacg agagacagca gctgggtggag 1140
acacacatgg ccagagtggg agccatgctc aatgaccgcc gccgcctggc cctgggagaac 1200
tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag 1260
aagtatgttc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320
cgcatgggtgg atcccaagaa agccgctcag atccgggtccc aggttatgac acacctccgt 1380
gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc 1440
gaggagattc aggatgaagt tgatgagctg cttcagaaaag agcaaaaacta ttcagatgac 1500
gtcttgggcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatggca 1560
tctttgaccg aaacgaaaac caccgtggag ctccctcccc tgaatggaga gttcagcctg 1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680
gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt 1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tggtctttgc agaagatgtg 1860
ggttcaaaca aaggtgcaat cattggactc atgggtgggcg gtgttggtcat agcgacagtg 1920
atcgatcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
gtggaggttg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

```

<210> 10

<211> 695

<212> PRT

<213> Homo sapiens

<400> 10

```

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1             5             10             15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
      20             25             30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
      35             40             45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
      50             55             60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
      65             70             75             80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
      85             90             95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
      100            105            110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
      115            120            125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
      130            135            140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
      145            150            155            160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
      165            170            175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
      180            185            190

```

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 11

<211> 2088

<212> DNA

<213> Homo sapiens

<400> 11

atgctgcccg	gtttggcact	gctcctgctg	gccgcctgga	cggctcgggc	gctggaggta	60
cccactgatg	gtaatgctgg	cctgctggct	gaaccccaga	ttgccatggt	ctgtggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaa	180
acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtcaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgatgccct	tctcgttcct	gacaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcactgg	cacaccgtcg	ccaaagagac	atgcagtga	480
aagagtacca	acttgcatga	ctacggcatg	ttgctgcctt	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcgga	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcca	ccaccaccac	caccaccaca	840
gagtcctgtg	aagaggtggt	tcgagttcct	acaacagcag	ccagtacccc	tgatgccgtt	900
gacaagtatc	tcgagacacc	tggggatgag	aatgaacatg	cccatttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcatgagaga	atgggaagag	1020
gcgaacgctc	aagcaaagaa	cttgccataa	gctgataaga	aggcagttat	ccagcatttc	1080
caggagaaag	tggaatcttt	ggaacaggaa	gcagccaacg	agagacagca	gctggtggag	1140

```

acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac 1200
tacatcacccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaaag 1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320
cgcatgggtg atcccaagaa agccgctcag atccgggtccc aggttatgac acacctccgt 1380
gtgatttatg agcgcataaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc 1440
gaggagattc aggatgaagt tgatgagctg ctccagaaaag agcaaaacta ttcagatgac 1500
gtccttgcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560
tctttgaccg aaacgaaaac caccgtggag ctccctcccc tgaatggaga gtccagcctg 1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680
gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt 1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
ggttcaaaca aagtgcaat cattggactc atgggtggcg gtgttgtcat agcgacagtg 1920
atcgatcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
gtggaggttg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

```

<210> 12
 <211> 695
 <212> PRT
 <213> Homo sapiens

<400> 12

```

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1              5              10              15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
      20              25              30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
      35              40              45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
      50              55              60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
      65              70              75              80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
      85              90              95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
      100              105              110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
      115              120              125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
      130              135              140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
      145              150              155              160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
      165              170              175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
      180              185              190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
      195              200              205

```

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540

```

<210> 13
<211> 2088
<212> DNA
<213> Homo sapiens

<400> 13
atgctgcccg gtttggcact gtcctgctg gccgcctgga cggctcgggc gctggaggt 60
cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
acctgcattg ataccaagga agccaacctg cagtatggcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtacca tccagaactg gtgcaagcgg 300
ggccgcgaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt 360
gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag 480
aagagtttca acttcgatga ctacggcatg ttgctgccct gcggaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgttga ttctgctgat 600
gcgaggagg atgactcgga tgtctggtgg ggaggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtcctggtg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt 900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960
gagaggcttg aggccaaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080
caggagaaa ggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag 1140
acacacatgg tccagatgga agccatgctc aatgaccgcc gcgcctggc cctggagaac 1200
tacatcaccg ctctgcaggc tgttctctct cggcctcgtc acgtgttcaa tatgctaaag 1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacacc taaagcattt cgagcatgtg 1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt 1380
gtgatttatg agcgcatgaa tcagttctct tccctgctct acaacgtgcc tgcagtggcc 1440
gaggagattc aggtatgaag tgatgagctg cttcagaaga agcaaaacta ttcagatgac 1500
gtcttgccca acatgattag tgaaccaagg atcagttacg gaaacatqtc tctcatqcca 1560

```

<210>	13
<211>	2088
<212>	DNA
<213>	Homo

<400> 13

atgctgcccg	gtttggcact	gctcctgctg	gccgcctgga	cggctcgggc	gctggaggtg	60
cccactgatg	gtaatgctgg	cctgctggct	gaaccccaga	ttgccatgtt	ctgtgggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaaa	180
acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtgcaagc	ccatccccac	tttgcgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgtgcctct	tctcgttcct	gacaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcactgg	cacaccgtcg	ccaaagagac	atgcagtgag	480
aagagtacca	acttgcatga	ctacggcatg	ttgctgccct	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcggg	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcca	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggtggg	tcgagttcct	acaacagcag	ccagtacccc	tgatgccggt	900
gacaagtatc	tcgagacacc	tggggatgag	aatgaacatg	cccattttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcatgagaga	atgggaagag	1020
gcagaacgtc	aagcaaaaga	cttgccataa	gctgataaga	aggcagttat	ccagcatttc	1080
caggagaaag	tggaaatctt	ggaacaggaa	gcagccaacg	agagacagca	gctggtggag	1140
acacacatgg	ccagagtgga	agccatgtct	aatgaccgcg	gccgcctggc	cctggagaac	1200
tacatcaccg	ctctgcaggc	tgttcctcct	cggcctcgtc	acgtgttcaa	tatgctaaag	1260
aagtatgtcc	gcgcagaaca	gaaggacaga	cagcacaccc	taaagcattt	cgagcatgtg	1320
cgcattgttg	atcccaagaa	agccgctcag	atccggtccc	aggttatgac	acacctccgt	1380
gtgatttatg	agcgcataaa	tcagttcttc	tcctctgtct	acaacgtgcc	tgcagtggcc	1440
gaggagattc	aggatgaagt	tgatgagctg	cttcagaaag	agcaaaacta	ttcagatgac	1500
gtcttggcca	acatgattag	tgaaccaagg	atcagttacg	gaaacgattc	tctcatgcca	1560

tctttgaccg aaacgaaaac caccgtggag ctcttccccg tgaatggaga gttcagcctg 1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680
gaagttgagc ctgttgatgc ccgccttgct gccgaccgag gactgaccac tgcaccaggt 1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
ggttcaaaca aaggtgcaat cattggactc atgggtggcg gtgttgtcat agcgacagtg 1920
atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
gtggaggttg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

<210> 14
<211> 695
<212> PRT
<213> Homo sapiens

<400> 14

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220
Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu	Ala	Asp	Asp	245	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	
								265	Thr	Glu	Arg	Thr	Thr	Ser	Ile	
Glu	Ala	Glu	Glu	260	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
								280	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
Ala	Thr	Thr	Thr	275	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
Val	Pro	Thr	Thr	290	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu
							295					300				
Glu	Thr	Pro	Gly	305	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys
						310					315					320
Glu	Arg	Leu	Glu	325	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg
										330					335	
Glu	Trp	Glu	Glu	340	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp
									345					350		
Lys	Lys	Ala	Val	355	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu
								360					365			
Gln	Glu	Ala	Ala	370	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala
							375					380				
Arg	Val	Glu	Ala	385	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn
						390					395					400
Tyr	Ile	Thr	Ala	405	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe
										410					415	
Asn	Met	Leu	Lys	420	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His
									425					430		
Thr	Leu	Lys	His	435	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala
								440					445			
Ala	Gln	Ile	Arg	450	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu
							455					460				
Arg	Met	Asn	Gln	465	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala
						470					475					480
Glu	Glu	Ile	Gln	485	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn
										490				495		
Tyr	Ser	Asp	Asp	500	Val	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser
									505					510		
Tyr	Gly	Asn	Asp	515	Ala	Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr
								520					525			
Val	Glu	Leu	Leu	530	Pro	Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln
							535					540				
Pro	Trp	His	Ser	545	Phe	Gly	Ala	Asp	Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn
						550					555					560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 15

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 15

atgctgtcccg	gtttggcact	gctcctgctg	gccgcctgga	cggctcgggc	gctggaggtg	60
cccactgatg	gtaatgctgg	cctgctggct	gaaccccaga	ttgccatgtt	ctgtggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggacccaa	180
acctgcattg	ataccaagga	aggcatccct	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcgaagc	agtgcgaagc	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360
ggagtttgtaa	gtgatgccct	tctcgttcct	gacaaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcactgg	cacaccgtcg	ccaaagagac	atgcagttag	480
aagagtagca	acttgcatga	ctacggcatg	ttgctgccct	gcggaattga	caagttccga	540
ggggtagagtt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgctgat	600
ggcggaggagg	atgactcggg	tgtctgggtg	ggcggagcag	acacagacta	tgcagatggg	660
agtagaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	gggtatgagg	tagâggaâag	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcca	ccaccaccac	caccaccaca	840
gagttctgtgg	aagaggtggt	tcgagttcct	acaacagcag	ccagtacccc	tgatgccgtt	900
gacaagtatc	tcgagacacc	tggggatgag	aatgaacatg	cccatttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcatgagaga	atgggaagag	1020
gcagaacgtc	aagcaaagaa	cttgccataa	gctgataaga	aggcagttat	ccagcatttc	1080
ccaggagaag	tcgaatcttt	ggaacaggaa	gcagccaacg	agagacagca	gctgggtggag	1140
acacacatgg	cggagagtga	agccatgctc	aatgaccgcc	gccgcctggc	cctggtgaac	1200
acatcacccg	ctctgcaggc	tgttcctcct	cggcctcgtc	acgtgttcaa	tatgtaaaag	1260
aagtatgtcc	gcgcagaaca	gaaggacaga	cagcacaccc	taaagcattt	cgagcatgtg	1320
cgcatggtgg	atcccaagaa	agccgctcag	atccggtccc	aggttatgac	acacctccgt	1380
gtgatttatg	agcgcatgaa	tcagtctctc	tccttgctct	acaacgtgcc	tgcagtggcc	1440
gaggagattc	aggatgaagt	tgatgagctg	cttcagaaag	agcaaaaacta	ttcagatgac	1500
ctctctggcca	acatgaattg	tgaaccaagg	atcagttacg	gaaacgatgc	tctcatgcca	1560
cttttgaccg	aaacgaaaaac	caccgtggag	ctccttcccg	tgaattggaga	gttcagcctg	1620
gacgatctcc	agccgtggca	ttcttttggg	gctgactctg	tgccagccaa	cacagaaaac	1680

gaagttgagc ctgttgatgc cgcacctgct gccgaccgag gactgaccac tcgaccaggt 1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tggtctttgc agaagatgtg 1860
ggttcaaaca aaggtgcaat cattggactc atgggtggcg gtgttgatcat agcgacagtg 1920
atcgatcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatgggtgtg 1980
gtggagggttg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag 2094

<210> 16
<211> 697
<212> PRT
<213> Homo sapiens

<400> 16

Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg
1				5					10					15	
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro
			20					25					30		
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
		35					40					45			
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp
		50				55					60				
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu
	65				70					75					80
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn
			85						90					95	
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val
			100					105					110		
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
		115					120					125			
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
	130					135					140				
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
	145				150					155					160
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
			165						170					175	
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
			180					185					190		
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
		195					200					205			
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
	210					215					220				
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
	225				230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
			245					250						255	

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 17

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 17

atgctgcccc	gtttggcact	gctcctgctg	gcgcctgga	cggctcgggc	gctggaggta	60
cccactgatg	gtaatgctgg	cctgctggct	gaaccccgaga	ttgccatggt	ctgtggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaaa	180
acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgaacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtgcgaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggg	360
gagtttgtaa	gtgatgcctt	tctcgttcct	gacaagtgca	aattctttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcaactg	cacaccgtcg	ccaaagagac	atgcagtga	480
aagagtacca	acttgcatga	ctacggcatg	ttgctgccct	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcgga	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcca	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggtggg	tgcagttcct	acaacagcag	ccagtaccct	tgatgccgtt	900
gacaagtatc	tgcagacacc	tggggatgag	aatgaacatg	cccatttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcatgagaga	atgggaagag	1020
gcagaacgtc	aagcaaagaa	cttgcctaaa	gctgataaga	aggcagttat	ccagcatttc	1080
caggagaaag	tggaatcttt	ggaacaggaa	gcagccaacg	agagacagca	gctggtggag	1140
acacacatgg	ccagagtggg	agccatgctc	aatgaccgcc	gccgcctggc	cctggagaac	1200
tacatcaccg	ctctgcaggc	tgttcctcct	cggcctcgtc	acgtgttcaa	tatgctaaaag	1260
aagtatgtcc	gcgcagaaca	gaaggacaga	cagcacaccc	taaagcattt	cgagcatgtg	1320
cgcattggtg	atcccaagaa	agccgctcag	atccgggtccc	aggttatgac	acacctccgt	1380
gtgattttatg	agcgcattga	tcagtctctc	tccctgctct	acaacgtgcc	tgcagtggcc	1440
gaggagattc	aggatgaagt	tgatgagctg	cttcagaaag	agcaaaaacta	ttcatgatgc	1500
gtcttgggcca	acatgattag	tgaaccaagg	atcagttacg	gaaacgatgc	tctcatgcca	1560
tctttgaccg	aaacgaaaac	caccgtggag	ctccttcccc	tgaatggaga	gttcagcctg	1620
gacgatctcc	agccgtggca	ttcttttggg	gctgactctg	tgccagccaa	cacagaaaac	1680
gaagttgagc	ctgttgatgc	ccgccttgct	gccgaccgag	gactgaccac	tcgaccaggt	1740
tctggggtga	caaatatcaa	gacggaggag	atctctgaag	tgaatctgga	tgcagaattc	1800

cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
 ggttcaaaca aaggtgcaat cattggactc atgggtggcg gtgttgatcat agcgacagtg 1920
 atcgtcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
 gtggagggtg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
 ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag 2094

<210> 18
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15
 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30
 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 19

<211> 2094

<212> DNA

<213> Homo sapiens

<400> 19

atgtgtgcccg	gtttggcact	gctcctgctg	gccgcctgga	cggctcgggc	gctggaggtta	60
cccactgatg	gtaatgctgg	cctgctggct	gaaccccaga	ttgccatgtt	ctgtgggcaga	120
ctgaacatcg	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaa	180
acctgcattg	ataccaagga	aggcatcctg	cagtatggcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcgaagc	agtgcaagac	ccatccccac	tttgtgatcc	ctaccgcgtg	cttagttggt	360
gagtttgtaa	gtgatgccct	tctcgttcct	gacaagtgca	aattctttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcaactgg	cacaccgtcg	ccaaagagac	atgcagttag	480
aaagatacca	acttgcatga	ctacggcatg	ttgctgccct	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaagaagt	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcggg	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcc	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggttgt	tcgagttcct	acaacagcag	ccagtacccc	tgatgccgtt	900
gacaagtatc	tcgagacacc	tgggtagtag	aatgaacatg	cccattttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcattgagaga	atgggaagag	1020
gcagaacgtc	aagcaaagaa	cttgccctaaa	gctgataaga	aggcagttat	ccagctatttc	1080
gaggagaaa	tgggaatttt	ggaacaggaa	gcagccaacg	agagacagca	gctggtggag	1140
gcacacatgg	ccagagtggg	agccatgctc	aatgaccgcc	gccgcctggc	cctggagaa	1200
acatcacccg	ctctgcaggc	tggtcctcct	cggcctcgtc	acgtgttcaa	tatgctaaag	1260
agtatgtcc	gcgcagaa	gaaggacaga	cagcacacc	taaaacattt	cgagcatgtg	1320
gcatggtgg	atcccaagaa	agccgctcag	atccggtccc	aggttatgac	acacctccgt	1380
tgattttatg	agcgcatgaa	tcagtctctc	tccctgctct	acaacgtgcc	tgcagtggcc	1440
gaggagattc	aggatgaatg	tgatgagctg	cttcagaaa	agcaaaacta	ttcagatgac	1500
ctcttgccca	acatgattag	tgaaccaagg	atcagttacg	gaaacgatgc	tctcatgcc	1560
ctttgaccg	aaacgaaaac	caccgtggag	ctccttcccc	tgaatggaga	gttcagcctg	1620
acgatctcc	agccgtggca	ttcttttggg	gctgactctg	tgcacgccc	cacagaaaac	1680
aaagttgagc	ctgttgatgc	ccgcctgct	gccgaccgag	gactgaccac	tcgaccaggt	1740
ctgggttga	caaatatcaa	gacggaggag	atctctgaag	tgaagatgga	tgcagaattc	1800
gacatgact	caggatatga	agttcatcat	caaaaattgg	tgttctttgc	agaagatgtg	1860
gtttcaaca	aaggtgcaat	cattggactc	atggtggggc	gtgttgtcat	agcgacagtg	1920
tcttcatca	ccttggtgat	gctgagaag	aaacagtaca	catccattca	tcatggtgtg	1980
tggaggttg	acgccgtgt	cacccagag	gagcgccacc	tgtccaagat	gcagcagaac	2040
gctacgaaa	atccaacct	caagttcttt	gagcagatgc	agaacaagaa	gtag	2094

```
<210> 20
<211> 697
<212> PRT
<213> Homo sapiens
```

<400> 20

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
 565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 21

<211> 1341

<212> DNA

<213> Homo sapiens

<400> 21

```
atggctagca tgactggtgg acagcaaagt ggtcgcggat ccaccagca cggcatccgg 60
ctgcccctgc gcagcggcct gggggggcgc cccctggggc tgcggctgcc cggggagacc 120
gacgaagagc ccgaggagcc cggccggagg ggcagctttg tggagatggt ggacaacctg 180
aggggcaagt cggggcaggg ctactacgtg gagatgaccg tgggcagccc cccgcagacg 240
ctcaacatcc tgggtggatac aggcagcagt aactttgcag tgggtgctgc cccccacccc 300
ttcctgcac gctactacca gaggcagctg tccagcacat accgggacct ccggaagggt 360
gtgtatgtgc cctacaccca gggcaagtgg gaaggggagc tgggcaccga cctggtaagc 420
atccccatg gcccacacgt cactgtgcgt gccaacattg ctgccatcac tgaatcagac 480
aagtctttca tcaacggctc caactgggaa ggcacacctg ggctggccta tgctgagatt 540
gccaggcctg acgactccct ggagcctttc tttgactctc tggtaaagca gaccacggt 600
cccaacctct tctccctgca cctttgtggt gctggcttcc ccctcaacca gtctgaagt 660
ctggcctctg tcggagggag catgatcatt ggaggtatcg accactcgct gtacacagg 720
agtctctggt atacacccat ccggcgggag tggattatg aggtcatcat tgtgcgggtg 780
gagatcaatg gacaggatct gaaaatggac tgcaaggagt acaactatga caagagcatt 840
gtggacagtg gcaccaccaa ccttcgtttg cccaagaaag tgtttgaagc tgcagtcaaa 900
tccatcaagg cagcctcctc cacggagaag ttcctgatg gtttctggct aggagagcag 960
ctggtgtgct ggcaagcagg caccaccctt tggaaacatt tcccagtcac ctactctac 1020
ctaattgggtg aggttaccaa ccagtccttc cgcacacca tccctccgca gcaataacctg 1080
cggccagtgg aagatgtggc cacgtcccaa gacgactgtt acaagtttgc catctcacag 1140
tcatccacgg gcactgttat gggagctgtt atcatggagg gcttctacgt tgtctttgat 1200
cgggcccga aacgaattgg ctttctgtc agcgcttgcc atgtgcacga tgagttcagg 1260
acggcagcgg tggaaggccc ttttgtcac ttggacatgg aagactgtgg ctacaacatt 1320
ccacagacag atgagtcag a
```

<210> 22

<211> 446

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln
1 5 10 15

His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu
20 25 30

Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly
35 40 45

Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser
 50 55 60
 Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr
 65 70 75 80
 Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala
 85 90 95
 Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser
 100 105 110
 Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly
 115 120 125
 Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly
 130 135 140
 Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp
 145 150 155 160
 Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala
 165 170 175
 Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp
 180 185 190
 Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu
 195 200 205
 Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val
 210 215 220
 Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly
 225 230 235 240
 Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile
 245 250 255
 Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys
 260 265 270
 Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu
 275 280 285
 Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala
 290 295 300
 Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln
 305 310 315 320
 Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val
 325 330 335
 Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile
 340 345 350
 Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr
 355 360 365
 Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly
 370 375 380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp
385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
435 440 445

<210> 23
<211> 1380
<212> DNA
<213> Homo sapiens

<400> 23
atggctagca tgactgggtgg acagcaaagt ggctcgcgat cgatgactat ctctgactct 60
ccgcgtgaac aggacggatc caccacgac ggcatccggc tgcccctgcg cagcggcctg 120
gggggcgccc cctgggggt gcggctgccc cgggagaccg acgaagagcc cgaggagccc 180
ggcgggaggg gcagctttgt ggagatgggt gacaacctga ggggcaagtc ggggcagggc 240
tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca 300
ggcagcagta actttgcagt ggggtgctgcc cccacccct tctgcatcg ctactaccag 360
aggcagctgt ccagcacata ccgggacctc cggaaggggtg tgtatgtgcc ctacaccag 420
ggcaagtggg aaggggagct gggcaccgac ctggttaagca tcccccatgg cccaacgtc 480
actgtgcgtg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc 540
aactgggaag gcatcctggg gctggcctat gctgagattg ccaggcctga cgactccctg 600
gagcctttct ttgactctct ggtaaagcag acccaggttc ccaacctctt ctccctgcac 660
ctttgtgggt ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggaggaggc 720
atgatcattg gaggtatcga ccactcgctg tacacaggca gtctctggta tacacccatc 780
cggcgggagt ggtattatga ggtcatcatt gtgcggggtg agatcaatgg acaggatctg 840
aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac 900
cttcgtttgc ccaagaaagt gtttgaagct gcagtcaaat ccatcaaggc agcctcctcc 960
acggagaagt tccctgatgg tttctggcta ggagagcagc tgggtgtgctg gcaagcaggc 1020
accacccctt ggaacatttt cccagtcac tcaactctacc taatgggtga ggttaccaac 1080
cagtccttcc gcatcaccat ccttcgcgag caataacctgc ggccagtgga agatgtggcc 1140
acgtcccaag acgactgta caagtttgcc atctcacagt catccacggg cactgttatg 1200
ggagctgtta tcatggaggg cttctacgtt gtctttgatc gggcccgaaa acgaattggc 1260
tttgcgtgca gcgcttgcca tgtgcacgat gagttcagga cggcagcggg ggaaggccct 1320
tttgtcacct tggacatgga agactgtggc tacaacattc cacagacaga tgagtcatga 1380

<210> 24
<211> 459
<212> PRT
<213> Homo sapiens

<400> 24
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15

Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
20 25 30

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg
35 40 45

Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly
50 55 60

Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	65	70	75	80
Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	85	90	95	
Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	100	105	110	
Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	115	120	125	
Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	130	135	140	
Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	145	150	155	160
Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	165	170	175	
Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	180	185	190	
Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	195	200	205	
Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	His	Leu	Cys	Gly	Ala	210	215	220	
Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	225	230	235	240
Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	245	250	255	
Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	260	265	270	
Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	275	280	285	
Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	290	295	300	
Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	305	310	315	320
Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	325	330	335	
Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	340	345	350	
Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	355	360	365	
Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	370	375	380	
Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	385	390	395	400

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
 405 410 415
 Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
 420 425 430
 Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
 435 440 445
 Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 450 455

<210> 25
 <211> 1302
 <212> DNA
 <213> Homo sapiens

<400> 25
 atgactcagc atggtattcg tctgccactg cgtagcgggc tgggtgggtgc tccactgggt 60
 ctgcgtctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 120
 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180
 gtgggcagcc ccccgagac gctcaacatc ctgggtggata caggcagcag taactttgca 240
 gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 300
 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 360
 ctgggcaccg acctggttaag catcccccat ggcccccaacg tcaactgtgcg tgccaacatt 420
 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 480
 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 540
 ctggttaaag agaccacgt tcccaacctc ttctccctgc acctttgtgg tgcctggctt 600
 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 660
 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 720
 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 780
 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 840
 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 900
 ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 960
 ttcccagtc tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1020
 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1080
 tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1140
 ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1200
 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1260
 gaagactgtg gctacaacat tccacagaca gatgagtcat ga 1302

<210> 26
 <211> 433
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly
 1 5 10 15
 Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu
 20 25 30
 Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
 35 40 45
 Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
 50 55 60
 Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
 65 70 75 80

Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	85	90	95
Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	100	105	110
Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	115	120	125
Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	130	135	140
Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	145	150	155
Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	165	170	175
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	180	185	190
Leu	His	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	195	200	205
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	210	215	220
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	225	230	235
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	245	250	255
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	260	265	270
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	275	280	285
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	290	295	300
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	305	310	315
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	325	330	335
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	340	345	350
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	355	360	365
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	370	375	380
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	385	390	395
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	405	410	415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
420 425 430

Ser

```
<210> 27
<211> 1278
<212> DNA
<213> Homo sapiens
```

<400>	27						
atggctagca	tgactggtgg	acagcaaatg	ggtcgcggat	cgatgactat	ctctgactct	60	
ccgctggact	ctggtatcga	aaccgcagga	tcttttgtgg	agatggtgga	caacctgagg	120	
ggcaagtccg	ggcagggtcta	ctacgtggag	atgaccgtgg	gcagccccc	gcagacgctc	180	
aacatcctgg	tggtatacagg	cagcagtaac	tttgacagtgg	gtgctgcccc	ccacccttc	240	
ctgcatcgct	actaccagag	gcagctgtcc	agcacatacc	gggacctccg	gaagggtgtg	300	
tatgtgccct	acaccaggg	caagtgggaa	ggggagctgg	gcaccgacct	ggtaagcatc	360	
ccccatggcc	ccaacgtcac	tgtgcgtgcc	aacattgctg	ccatcactga	atcagacaag	420	
ttcttcatca	acgggtccaa	ctgggaaggg	atcctggggc	tggcctatgc	tgagattgcc	480	
aggcctgacg	actccctgga	gcctttcttt	gactctctgg	taaaggacag	ccaggttccc	540	
aacctcttct	ccctgcacct	ttgtggtgct	ggcttcccc	tcaaccagtc	tgaagtgctg	600	
gcctctgtcg	gagggagcat	gatcatttga	ggtatcgacc	actcgctgta	cacaggcagt	660	
ctctggtata	cacccatccg	gcgggagtg	tattatgagg	tcattcattgt	gcgggtggag	720	
atcaatggac	aggatctgaa	aatggactgc	aaggagtaca	actatgacaa	gagcattgtg	780	
gacagtgcca	ccaccaacct	tcgtttgccc	aagaaagtgt	ttgaagctgc	agtcaaatcc	840	
atcaaggcag	cctcctccac	ggagaagttc	cctgatggtt	tgtggttagg	agagcagctg	900	
gtgtgctggc	aagcaggcac	caccccttgg	aacattttcc	cagtcacttc	actctacctc	960	
atgggtgagg	ttaccaacca	gtccttccgc	atcaccatcc	ttccgcagca	atacctgcgg	1020	
ccagtggaag	atgtggccac	gtcccaagac	gactgttaca	agtttgccat	ctcacagtca	1080	
tccacgggca	ctgttatggg	agctgttatc	atggagggct	tctacgttgt	ctttgatcgg	1140	
gcccgaaaac	gaattgctt	tgctgtcagc	gcttgccatg	tgcacgatga	gttcaggacg	1200	
gcagcggtgg	aaggcccttt	tgtcaccttg	gacatggaag	actgtggcta	caacattcca	1260	
cagacagatg	agtcatga					1278	

```
<210> 28
<211> 425
<212> PRT
<213> Homo sapiens
```

```

<400> 28
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
  1          5          10          15
Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe
          20          25          30
Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr
          35          40          45
Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
          50          55          60
Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe
  65          70          75          80
Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
          85          90          95
Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
          100          105          110
Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
          115          120          125

```

Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn
130 135 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala
145 150 155 160

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln
165 170 175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe
180 185 190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile
195 200 205

Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr
210 215 220

Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu
225 230 235 240

Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp
245 250 255

Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys
260 265 270

Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu
275 280 285

Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln
290 295 300

Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu
305 310 315 320

Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln
325 330 335

Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys
340 345 350

Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala
355 360 365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg
370 375 380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr
385 390 395 400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly
405 410 415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425

<210> 29
<211> 1362
<212> DNA
<213> Homo sapiens

<400> 29

atggcccaag	ccctgccttg	gctcctgctg	tggatggggc	cgggagtgt	gcctgcccac	60
ggcaccacag	acggcatccg	gctgcccttg	cgcagcggcc	tggggggcgc	ccccctgggg	120
ctgcggctgc	cccgggagac	cgacgaagag	cccaggagac	ccggccggag	gggcagcttt	180
gtggagatgg	tggacaacct	gagggggcaag	tcggggcagg	gctactacgt	ggagatgacc	240
gtgggcagcg	ccccgcagac	gctcaacatc	ctggtggata	caggcagcag	taactttgca	300
gtgggtgctg	ccccccacc	cttctgcat	cgctactacc	agaggcagct	gtccagcaca	360
taccggggacc	tccggaaggg	tgtgtatgtg	ccctacaccc	agggcaagt	ggaaggggag	420
ctgggacacc	acctggtaa	catccccat	ggccccaacg	tactgtgcg	tgccaaatt	480
gctgccatca	ctgaatcaga	caagttcttc	atcaacggct	ccaactggga	aggcatcctg	540
gggtctggct	atgtgagat	tgcaggcct	gacgactccc	tggagccttt	ctttgactct	600
ctggtaaagc	agaccacgt	tcccaacct	tctccctgc	acctttgtgg	tgtgtgcttc	660
ccctcaacc	agtctgaagt	gctggcctct	gtcggaggga	gcatgatcat	tggaggtatc	720
gaccactcgc	tgtacacagg	cagtctctgg	tatacaccca	tccggcggga	tgggtattat	780
gaggtcatca	ttgtgcgggt	ggagatcaat	ggacaggatc	tgaaaatgga	ctgcaaggag	840
tacaactatg	acaagagcat	tgtggacagt	ggcaccacca	accttcgttt	gcccaagaaa	900
gtgtttgaag	ctgcagtcaa	atccatcaag	gcagcctcct	ccacggagaa	gttccctgat	960
ggtttctggc	taggagagca	gctggtgtgc	tggcaagcag	gcaccacccc	ttggaacatt	1020
ttcccagtc	tctactcta	cctaattgggt	gaggttacca	accagtcctt	ccgcataccc	1080
atccttccgc	agcaataacct	gcggccagtg	gaagatgtgg	ccacgtccc	agacgactgt	1140
tacaagtttg	ctatctcaca	gtcatccacg	ggcactgtta	tgggagctgt	tatcatggag	1200
ggcttctacg	ttgtctttga	tcggggccga	aaacgaattg	gctttgtgtg	cagcgttgc	1260
catgtgcacg	atgagttcag	gacggcagcg	gtggaaggcc	ctttgtgcac	cttggacatg	1320
gaagactgtg	gctacaacat	tccacagaca	gatgagtc	ga		1362

<210> 30

<211> 453

<212> PRT

<213> Homo sapiens

<400> 30

Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5					10				15	
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg Ser
			20					25					30	
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr Asp
		35					40					45		
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met Val
	50					55					60			
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met Thr
65					70					75				80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly Ser
				85					90					95
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg Tyr
			100					105					110	
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly Val
		115					120					125		
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr Asp
	130					135					140			
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn Ile
145					150					155				160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser
450

<210> 31
<211> 1380
<212> DNA

<213> Homo sapiens

<400> 31

```

atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgtt gcctgcccac 60
ggcaccacag acggcatccg gctgcccctg cgcagcggcc tgggggggag cccctggggg 120
ctgagggtgc cccgggagac cgacgaagag cccgaggagc cgggcccagg gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctgggtggata caggcagcag taactttgca 300
gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctgggcaccg acctggtaag catcccccat ggcccacaacg tcactgtgag tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatactg 540
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
ctggtaaagc agaccacagt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
cccctcaacc agtctgaagt gctggcctct gtccggaggga gcatgatcat tggaggtatc 720
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
ggtttctggc taggagagca gctgggtgtg tggcaagcag gcaccacccc ttggaacatt 1020
ttcccagtc tctcactcta cctaattggg gaggttacca accagtcctt ccgcatcacc 1080
atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1200
ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga 1380

```

<210> 32

<211> 459

<212> PRT

<213> Homo sapiens

<400> 32

```

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
  1                      5                      10                      15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
      20                      25                      30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
      35                      40                      45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
      50                      55                      60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
      65                      70                      75                      80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
      85                      90                      95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
      100                      105                      110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
      115                      120                      125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
      130                      135                      140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
      145                      150                      155                      160

```



<212> PRT
<213> Homo sapiens

<400> 33
Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu
1 5 10 15
Ser Ser Leu Val Arg His Arg Trp Lys
20 25

<210> 34
<211> 19
<212> PRT
<213> Homo sapiens

<400> 34
Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
1 5 10 15
Leu Leu Lys

<210> 35
<211> 29
<212> DNA
<213> Homo sapiens

<400> 35
gtggatccac ccagcacggc atccggctg 29

<210> 36
<211> 36
<212> DNA
<213> Homo sapiens

<400> 36
gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 37
<211> 39
<212> DNA
<213> Homo sapiens

<400> 37
gatcgatgac tatctctgac tctccgcgtg aacaggacg 39

<210> 38
<211> 39
<212> DNA
<213> Homo sapiens

<400> 38
gatccgtcct gttcacgcgg agagtcagag atagtcac 39

<210> 39
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hu-Asp2

<400> 39
 cggcatccgg ctgcccctgc gtagcgggtct ggggtgggtgct ccactggggtc tgcgtctgcc 60
 ccgggagacc gacgaag 77

<210> 40
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hu-Asp2

<400> 40
 cttcgtcggg ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60
 ggggcagccg gatgccg 77

<210> 41
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase 8
 Cleavage Site

<400> 41
 gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase 8
 Cleavage Site

<400> 42
 gatccgtcgg ttccgatacc agagtccagc ggagagtcag agatagtcac c 51

<210> 43
 <211> 32
 <212> DNA
 <213> Homo sapiens

<400> 43
 aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 44
 gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 45
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 6-His tag

<400> 45		
gatcgcatca tcacatcac catg		24
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: 6-His tag		
<400> 46		
gatccatggt gatggtgatg atgc		24
<210> 47		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: primer		
<400> 47		
gactgaccac tcgaccaggt tc		22
<210> 48		
<211> 51		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: primer		
<400> 48		
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c		51
<210> 49		
<211> 26		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: primer		
<400> 49		
cgaattaaat tccagcacac tggcta		26
<210> 50		
<211> 1287		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Hu-Asp2(b) delta TM		
<400> 50		
atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgtct gcctgcccac 60		
ggcaccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120		
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180		
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240		
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300		
gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360		

```

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctggggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
gggctggcct atgtgagat tgccaggctt tgtgggtgtg gcttccccct caaccagtct 600
gaagtgtggg cctctgtcgg agggagcatg atcattggag gtatcgacca ctcgctgtac 660
acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca 840
gtcaaatacca tcaaggcagc ctctccacg gagaagttcc ctgatggttt ctggctagga 900
gagcagctgg tgtgctggca agcaggcacc accccttggg acattttccc agtcattctca 960
ctctacctaa tgggtgaggt taccaaccag tccttcgca tcaccatcct tccgcagcaa 1020
tacctgcggc cagtggaaga tgtggccacg tcccaagacg actgttataa gtttgccatc 1080
tcacagtcac ccacgggcac tggtatggga gctgttatca tggagggctt ctacgttgct 1140
tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
ttcaggacgg cagcgggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
aacattccac agacagatga gtcatga 1287

```

<210> 51

<211> 428

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
delta TM

<400> 51

```

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
  1                      5                      10                      15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
          20                      25                      30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
          35                      40                      45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
          50                      55                      60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
          65                      70                      75                      80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
          85                      90                      95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
          100                      105                      110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
          115                      120                      125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
          130                      135                      140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
          145                      150                      155                      160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
          165                      170                      175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
          180                      185                      190

```

- 44 -

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 420 425

<210> 52

<211> 1305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hu-Asp2(b)
 delta TM

<400> 52

```

atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgct gcctgccac 60
ggcaccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120
ctgaggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc cccgcagac gctcaacatc ctgggtggata caggcagcag taactttgca 300
gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420

```

```
<210> 53
<211> 434
<212> PRT
<213> Artificial Sequence
```

<400> 53
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His
 420 425 430

His His

<210> 54
 <211> 2310
 <212> DNA
 <213> Homo sapiens

<400> 54
 atgctgcccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
 cccactgatg gtaatgctgg cctgctggct gaacccaga ttgccatgt ctgtggcaga 120
 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180
 acctgcattg ataccaagga aggcacctg cagtattgcc aagaagtcta ccctgaactg 240
 cagatcacca atgtggtaga agccaaccaa ccagtgaacca tccagaactg gtgcaagcgg 300
 ggccgcaagc agtgcaagac ccatcccccac tttgtgattc cctaccgctg cttagttggt 360

```
<210> 55
<211> 770
<212> PRT
<213> Homo sapiens
```

```

<400> 55
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
  1           5           10           15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
          20           25           30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
          35           40           45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
      50           55           60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
      65           70           75           80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
          85           90           95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
          100          105          110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
      115          120          125

```

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu	Asn	Asp	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu
465														480
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys
				485					490					495
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His
			500					505					510	Phe
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg
		515					520					525		Ser
Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln
	530					535					540			Ser
Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	Glu	Glu	Ile	Gln
545					550					555				560
Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp
				565					570					575
Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	Tyr	Gly	Asn	Asp
			580					585					590	Ala
Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	Val	Glu	Leu	Leu
		595					600					605		Pro
Val	Asn	Gly	Glu	Phe	Ser	Leu	Asp	Asp	Leu	Gln	Pro	Trp	His	Ser
	610						615				620			Phe
Gly	Ala	Asp	Ser	Val	Pro	Ala	Asn	Thr	Glu	Asn	Glu	Val	Glu	Pro
625					630					635				640
Asp	Ala	Arg	Pro	Ala	Ala	Asp	Arg	Gly	Leu	Thr	Thr	Arg	Pro	Gly
				645					650					655
Gly	Leu	Thr	Asn	Ile	Lys	Thr	Glu	Glu	Ile	Ser	Glu	Val	Lys	Met
			660					665					670	Asp
Ala	Glu	Phe	Arg	His	Asp	Ser	Gly	Tyr	Glu	Val	His	His	Gln	Lys
		675					680					685		Leu
Val	Phe	Phe	Ala	Glu	Asp	Val	Gly	Ser	Asn	Lys	Gly	Ala	Ile	Ile
	690					695					700			Gly
Leu	Met	Val	Gly	Gly	Val	Val	Ile	Ala	Thr	Val	Ile	Val	Ile	Thr
705					710					715				720
Val	Met	Leu	Lys	Lys	Lys	Gln	Tyr							

<400> 56

<210> 57

<211> 751

<212> PRT

<213> Homo sapiens

<400> 57

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335
 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350
 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365
 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
 370 375 380
 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
565 570 575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

```

<400> 59
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
  1                    5              10              15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
    20              25              30

```

- 54 -

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

- 55 -

<400> 60						
atgctgccccg	gtttggcact	gctcctgctg	gccgcctgga	cggctcgggc	gctggaggtta	60
cccactgatg	gtaatgctgg	cctgctgggt	gaacccaga	tgccatggt	ctgtggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggacaaa	180
acctgcattg	ataccaagga	aggcatactg	cagtatggc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtgaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgatgccct	tctcgttcc	gacaagtga	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcaactg	cacaccgtcg	ccaaagagac	atgcagttag	480
aagagtacca	acttgcatga	ctacggcatg	ttgctgccct	gcggaatgga	caagttccga	540
ggggtagaggt	ttgtgtgttg	ccactgggt	gaagaaagt	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcgga	tgtctggttg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggtcgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcc	ccaccaccac	caccaccaca	840
gagctctgtg	aagaggtggg	tcgagaggtg	tgctctgaac	aagccgagac	ggggccgtgc	900
cgagcaatga	tctccgctg	gtactttgat	gtgactgaag	ggaagtgtgc	ccattctttt	960
tacggcggat	gtggcggcaa	ccggaacaac	tttgacacag	aagagtactg	catggccgtg	1020
tgtggcagcg	ccattcctac	aacagcagcc	agtaccctg	atgccgttga	caagtatctc	1080
gagacacctg	gggatgagaa	tgaacatgcc	catttccaga	aagccaaaga	gaggcttgag	1140
gccaaagcacc	gagatgaga	gtcccaggtc	atgagagaat	gggaagaggc	agaactcaa	1200
gcaaagaact	rgcctaagc	tgataagaag	gcagttatcc	agcatttcca	ggagaaagtg	1260
gaatctttgg	aacaggaagc	agccaacgag	agacagcagc	tggtggagac	acacatggcc	1320
agagtggaa	ccatgctcaa	tgaccgcgc	cgcttgccc	tggaagacta	catcaccgct	1380
ctgcaggctg	ttcctcctcg	gcctcgtcac	gtgttcaata	tgctaaagaa	gtatgtccgc	1440
gcgaacaga	aggacagaca	gcacacccta	aagcatttgc	agcatgtgcg	catgggtggat	1500
ccaaagaag	ccgctcagat	ccggtcccag	gttatgacac	acctccgtgt	gatttatgag	1560
cgcataatc	agtctctctc	cctgctctac	aacgtgcctg	cagtggccga	ggagattcag	1620
gatgaagtgt	atgagctgct	tcagaaagag	caaaactatt	cagatgacgt	cttggccaac	1680
atgattagt	aaccaaggat	cagttacgga	aacgatgtc	tcatgccatc	tttgaccgaa	1740
acgaaaaacca	ccgtggagct	ccttcccgtg	aatggagagt	tcagcctgga	cgatctccag	1800
ccgtggcatt	cttttggggc	tgactctgtg	ccagccaaca	cagaaaacga	agttgagcct	1860
gttgatgccc	gccctgctgc	cgaccgagga	ctgaccactc	gaccaggttc	tggtgtgaca	1920
aatatcaaga	cggaggagat	ctctgaagt	aagatggatg	cagaattccg	acatgactca	1980
ggatatgaag	ttcatcatca	aaaattggtg	ttctttgcag	aagatgtggg	ttcaaaaaa	2040
gggtgcaatca	ttggactcat	ggtgggcggt	gttgtcatag	cgacagtgat	cgatcatcacc	2100
ttgggtgatg	tgaagaagaa	acagtacaca	tccattcacc	atgggtgtgt	ggaggttgac	2160
gccgctgtca	ccccagagga	gcgcacactg	tccaagtgc	agcagaacgg	ctacgaaaat	2220
ccaacctaca	agttctttga	gcagatgcag	aacaagaag			2259

<210> 61
 <211> 753
 <212> PRT
 <213> Homo sapiens

<400> 61
 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15
 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30
 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
565 570 575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys
740 745 750

Lys

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 62
Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 63
Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5 10

<210> 64
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 64
Ser Glu Val Lys Met Asp Ala Glu Phe Arg
1 5 10

<210> 65
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 65
Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg
1 5 10 15

<210> 66
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 66
Asn Leu Asp Ala
1

<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 67
Glu Val Lys Met Asp Ala Glu Phe
1 5

<210> 68
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 68
Gly Arg Arg Gly Ser
1 5

<210> 69
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 69

Thr Gln His Gly Ile Arg
1 5

 $\langle 210_H \rangle = 70$

~~<211>~~ 6

<212> PRT

~~<213>~~ Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Peptide

$\langle 400 \rangle$ 70

Glu Thr Asp Glu Glu Pro
1 5

<210> 71

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

<400> 71

Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro
1 5 10 15

<210> 72

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 72

Asp Ala Glu Phe Arg
1 5

<210> 73

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic

<400> 73

Ser Glu Val Asn Leu
1 5